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Understanding dengue transmission and risk factors through ecohealth approach in Bangladesh

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Background: Southeast Asian countries including Bangladesh have remained hyperendemic for dengue due to unplanned urbanization, overcrowding, poverty and health inequalities. In recognition of the need for an multidisciplinary, scientific research on this problem, we applied an "Ecohealth Approach" to understand dengue virus (DENV) transmission and social-ecological risk factors in Dhaka, Bangladesh.

Methods & Materials: Multiple disciplinary aspects were encapsulated by examination of: i) rates of human exposure to DENV by identifying individuals (via a serosurvey in 1200 households and 47 clinical samples) with IgM and IgG antibodies to DENV; ii) abundance of dengue vector during monsoon and dry seasons in the same households; iii) self-risk perception by the community members; and iv) human organizations responsible for interventions. Data included in the analysis are: a) two vector surveys [i.e., pupal surveys conducted in 847 households (monsoon season 2011) and 459 households (dry season 2012)]; b) two serosurveys [i.e., serosurveys conducted in 1128 households (pre monsoon season 2012) and 1130 households (630 paired sera and 500 replacement sera during post monsoon season 2012)]; c) socio-demographic survey of 300 households; and d) 12 focus group discussions and 12 key informant interviews.

Results: Competent dengue vectors were detected in > 40% and 12% of households during the monsoon and dry seasons respectively. The monsoon and dry seasonal pupal index were 0.40 and 0.33 respectively for the selected 12 wards. Only 8 types of key containers and two types of ecological clusters are responsible for 72% of pupal distribution. More than 80% IgG and nearly 3% IgM were positive during pre- and post-monsoon serosurvey. Among the IgM positives, in-house PRNTs, using a serial dilution of sera mixed with a DENV serotype, are being carried out. There are significant variations in dengue risk perception between lower and higher socioeconomic groups. Also, experts ranked dengue risk at a much lower level than lay persons and experts emphasized the need for stronger institutional measures to control dengue outbreaks.

Conclusion: The overall findings of the study will contribute to the advancement of DENV transmission knowledge, forecast the disease burden as well as socioeconomic burden in the City of Dhaka,Bangladesh.

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Dengue virus surveillance in a medium size city in Brazil reveals a complex pattern of serotypes and strains circulation

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Background: Dengue viruses are members of the genus *Flavivirus* in the family *Flaviviridae* and cover 4 antigenically distinct serotypes. The emergence of epidemic dengue in the Americas, as well as worldwide, has been characterized by a rise to hyperendemicity. In the present work we looked the Dengue viruses transmission in Sao Jose do Rio Preto (a 400K habitants city in Sao Paulo state, Brazil) from 2011 to 2013.

Methods & Materials: We used serum samples of suspected and confirmed DENV patients provided by the Public Health Authority to profile DENV circulation. The viral surveillance was performed with multiplex RT-PCR using *Flavivirus* generic primers based on non-structural protein (NS5), followed by nested assays with species-specific primers. We analyzed 704 cases from August 2011 to July 2013.

Results: with species-specific primers. We analyzed 704 cases from August 2011 to July 2013. We amplified 585 samples for DENV and 80 (13,5%) were positive for DENV-1, 65 (11%) DENV-2, 437 (75%) DENV-4 and 3 (0,5%) DENV-1/DENV-4 coinfection, showing a complex pattern of serotypes circulation. Up to now, 14 DENV-1, 15 DENV-2 and 31 DENV-4 have been subjected to sequencing of the entire envelope gene or full genome (using next generation sequencing) and were used for phylogenetic reconstruction. The three phylogenetic analyses of serotypes 1, 2 and 4 show that the samples identified in this study grouped with genotypes that circulating in Brazil (genotypes V, Asian American and American, for types 1, 2 and 4 respectively). Looking inside the genotypes two distinct clades formed in DENV-1 phylogenetic reconstructions, indicating two possible lineages. For DENV-2 and DENV-4, one clade grouped all SJRP samples, indicating a single possible lineage.

Conclusion: This data shows that the phylodinamics of dengue circulation can be much more complex than expected even in a small city, with circulation not only of different serotypes but also different strains as we already showed before for DNEV-3. These data provide us more information about the dynamics of DENV circulation and its role in emergence of outbreaks and endemic circulation.

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